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(b) at least one intron sequence, wherein said intron sequence is selected from the group of hMSH5 introns consisting of SEQ. ID NOS:55-85.

Please add the following claims:

-- 46. The isolated and purified nucleic acid of claim 3, further comprising a radioactive label or a fluorescent tag.

F4 47. The isolated and purified nucleotide segment of claim 41, further comprising a radioactive label or fluorescent tag.

48. The isolated nucleotide segment of claim 3, wherein said fragments are selected from nucleotides 235-1908 of SEQ ID NO:1.

49. The isolated nucleotide segment of claim 44, wherein said fragments are between nucleotides 235-1908 of SEQ ID NO:1. --

REMARKS

A comparison between the pending claims and the claims as amended is set forth in the attached Appendix.

Applicants have amended claims 3 and 41 to expedite prosecution. The amendment removes an objected to recitation. Applicants further amended claims 3 to specify that the fragment is from the coding region. This is supported throughout the specification. See particularly pages 35-43, particularly page 41. The amendments to claims 41 and 46 are editorial in nature. The amendment to claim 45 corrects some typographical errors and is otherwise editorial in nature.

New claims 46 and 47 are both supported by the specification at page 43, second full paragraph. As such, these amendments do not constitute new matter and their entry is respectfully requested.

Applicants appreciate the Examiner's indication that claims 2, 4, 39 40 and 42 are allowed.

Claims 3, 6-8, 10, 12, 41 and 44 were however rejected under 35 U.S.C. § 112, first paragraph. Claims 48 and 49 are supported by the specification at pages 51-52.

It is the Examiner's contention that the recitation in claim 3 "cannot be selected only from basepairs in 1908-2900" represents new matter. The Examiner has, however, indicated that the specification provides basis for claims to fragments selected from nucleotides 1- 1901 of SEQ ID NO:1. While applicants disagree with the Examiner's rejection, such a recitation is not necessary and in order to expedite prosecution has been eliminated from the claims. Thus, the rejection has been obviated.

Claim 45 was rejected under 35 USC 112, second paragraph.

Applicants have amended the claim to correct a typographical error where exon 1 was not explicitly identified and have eliminated the phrase "combination thereof" because as the Examiner points

out the claim uses the phrase "at least one" and the phrase was superfluous. As a result of this amendment, this rejection has been obviated.

Claims 3, 6, 8, 41 and 44 were rejected under 35 U.S.C. § 102(b) as being anticipated by Cross et al.

Applicants respectfully submit that this rejection should be withdrawn for the following reasons. The Cross sequence does not overlap with any coding region of the present application.

As taught at page 54, lines 11-12, the translational start is base 235 with the translational stop at base 2737. Accordingly, there could never be any overlap for claims such as claim 42 wherein said nucleotide segment was restricted to mRNA or cDNA as the portion of SEQ ID NO:1 that the Cross sequence matches up to would not be in this region. Thus, there could not be an anticipation with respect to claim 41 as by definition the cDNA and mRNA start at the coding region. The amendment to claim 3 to specify that the fragment is from the coding region of SEQ ID NO: 1 has avoided any incidental overlap with respect to this claim. Thus, this rejection should be withdrawn.


Applicant believes that no extension of term is required. However, this conditional petition is being made to provide for the possibility that applicant has inadvertently overlooked the need for a petition for extension of time. If any additional extension and/or fee is required, charge Account No. 50-0850.

In view of the foregoing, applicants respectfully submit that all claims are in condition for allowance. Early and favorable action is requested.

Respectfully submitted,

Date

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VERSION TO SHOW MARKED CHANGES IN CLAIMS

3. An isolated nucleotide segment of no more than 3000 nucleotides containing a fragment of at least 17 contiguous nucleotides from the coding region as set forth in SEQ ID NO:1[, with the exception that said fragment cannot be selected only from base pairs 1908-2900].

41. An isolated and purified nucleotide segment, wherein said nucleotide segment is a fragment of at least 17 contiguous nucleotides of SEQ ID NO: 1, [with the exception that said fragment cannot be selected only from base pairs 1908-2900,] and wherein said nucleotide segment is mRNA or cDNA.

44. The isolated [and purified nucleic acid segment] nucleotide segment of claim 3, wherein said nucleotide segment consists of said fragments of SEQ ID NO:1.

45. An isolated and purified nucleotide SEQ segment consisting of

(a) at least one exon from SEQ ID NO:1 wherein starting at position 235 and continuing continuously, exon 1 is 221 basepairs, exon 2 is the next 160 basepairs, exon 3 is the next 124 basepairs, exon 4 is the next 81 basepairs, exon 5 is the next 63 basepairs, exon 6 is the next 122 basepairs, exon 7 is the next 110 basepairs, exon 8 is the next 36 basepairs, exon 9 is the next 83 basepairs, exon 10 is the next 46 basepairs, exon 11 is the next 139 basepairs, exon 12 is the next 63 basepairs, exon 13 is the next 129 basepairs, exon 14 is the next 73 basepairs, exon 15 is the next 110 basepairs, exon 16 is the next 81 basepairs, exon 17 is the next 88 basepairs, exon 18 is the next 190 basepairs, exon 19 is the next 127 basepairs, exon 20 is the next 150 basepairs, exon 21 is the next 75 basepairs, exon 22 is the next 144 basepairs, exon 23 is the next 138 basepairs, exon 24 is the next 74 basepairs, and exon 25 is the next 254 basepairs;

(b) at least one intron sequence, wherein said intron sequence is selected from the group of hMSH5 introns consisting of SEQ. ID NOS:55-85 [and combinations thereof].